



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 175936

TO: Mary K Zeman
Location: REM/2D61/2C70
Art Unit: 1631
Thursday, January 19, 2006

Case Serial Number: 10/655870

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Zeman,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

Filed 9/5/03
No Prior/Prior art

new drawings 1/27/04 OK
IDS 4/7/04

Purvis, G

Claims 1-10, 31
System, no hardware
Not concrete, tangible, useful 101

11-20
Method. Not CIP, 101
21-30
Software embodied.

31- means + function
System 112
No hardware
Structure in spec?

=> d his ful

(FILE 'HOME' ENTERED AT 17:54:45 ON 19 JAN 2006)

FILE 'HCAPLUS' ENTERED AT 17:54:53 ON 19 JAN 2006

E PURVIS GEORGE

E PURVIS GEORGE/AU

L1 73 SEA ABB=ON ("PURVIS G G"/AU OR "PURVIS G H"/AU OR "PURVIS
GEORGE"/AU OR "PURVIS GEORGE A"/AU OR "PURVIS GEORGE D"/AU OR
"PURVIS GEORGE D III"/AU)
L2 2 SEA ABB=ON L1 AND ?PROTEIN?(W)?LIGAND?
L3 ANALYZE L2 1-1 CT : 14 TERMS

FILE 'HCAPLUS' ENTERED AT 18:01:51 ON 19 JAN 2006

L4 1965 SEA ABB=ON ?POTENTIAL?(3W)?MEAN?(W)?FORCE? OR PMF
L5 26 SEA ABB=ON L4 AND ?PROTEIN?(W)?LIGAND?
L6 4 SEA ABB=ON L5 AND (?REPULS? OR ?PAIR? OR ?INTERATOM?)(W)?POTEN
T?
L7 2 SEA ABB=ON L6 AND (PRD<20030905 OR PD<20030905)

FILE 'MEDLINE, BIOSIS, EMBASE, JAPIO, JICST-EPLUS, COMPENDEX' ENTERED AT
18:04:25 ON 19 JAN 2006

L8 3 SEA ABB=ON L6
L9 1 DUP REMOV L8 (2 DUPLICATES REMOVED)

FILE 'USPATFULL' ENTERED AT 18:05:53 ON 19 JAN 2006

L10 3 SEA ABB=ON L6 AND (PRD<20030905 OR PD<20030905)

FILE HOME

FILE HCAPLUS

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FILE COVERS 1907 - 19 Jan 2006 VOL 144 ISS 4
FILE LAST UPDATED: 18 Jan 2006 (20060118/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

FILE MEDLINE

FILE LAST UPDATED: 19 JAN 2006 (20060119/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 will soon be available. For details on the 2005 reload, enter HELP RLOAD at an arrow prompt (=>).
See also:

<http://www.nlm.nih.gov/mesh/>

http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html
http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate

FILE BIOSIS

FILE COVERS 1969 TO DATE.

CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 19 January 2006 (20060119/ED)

FILE EMBASE

FILE COVERS 1974 TO 12 Jan 2006 (20060112/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

This file contains CAS Registry Numbers for easy and accurate
substance identification.

FILE JAPIO

FILE LAST UPDATED: 02 JAN 2006 <20060102/UP>

FILE COVERS APR 1973 TO SEPTEMBER 29, 2005

>>> GRAPHIC IMAGES AVAILABLE <<<

>>> NEW IPC8 DATA AND FUNCTIONALITY NOT YET AVAILABLE IN THIS FILE.
USE IPC7 FORMAT FOR SEARCHING THE IPC. WATCH THIS SPACE FOR FURTHER
DEVELOPMENTS AND SEE OUR NEWS SECTION FOR FURTHER INFORMATION
ABOUT THE IPC REFORM <<<

FILE JICST-EPLUS

FILE COVERS 1985 TO 18 JAN 2006 (20060118/ED)

THE JICST-EPLUS FILE HAS BEEN RELOADED TO REFLECT THE 1999 CONTROLLED
TERM (/CT) THESAURUS RELOAD.

FILE COMPENDEX

FILE LAST UPDATED: 16 JAN 2006 <20060116/UP>

FILE COVERS 1970 TO DATE.

<<< SIMULTANEOUS LEFT AND RIGHT TRUNCATION AVAILABLE IN
THE BASIC INDEX >>>

FILE USPATFULL

FILE COVERS 1971 TO PATENT PUBLICATION DATE: 19 Jan 2006 (20060119/PD)

FILE LAST UPDATED: 19 Jan 2006 (20060119/ED)

HIGHEST GRANTED PATENT NUMBER: US6988280

HIGHEST APPLICATION PUBLICATION NUMBER: US2006015978

CA INDEXING IS CURRENT THROUGH 19 Jan 2006 (20060119/UPCA)

ISSUE CLASS FIELDS (/INCL) CURRENT THROUGH: 19 Jan 2006 (20060119/PD)

REVISED CLASS FIELDS (/NCL) LAST RELOADED: Oct 2005

USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Oct 2005

=> d que stat 17

L4 1965 SEA FILE=HCAPLUS ABB=ON ?POTENTIAL?(3W)?MEAN?(W)?FORCE? OR
PMF
L5 26 SEA FILE=HCAPLUS ABB=ON L4 AND ?PROTEIN?(W)?LIGAND?
L6 4 SEA FILE=HCAPLUS ABB=ON L5 AND (?REPULS? OR ?PAIR? OR
?INTERATOM?) (W)?POTENT?
L7 2 SEA FILE=HCAPLUS ABB=ON L6 AND (PRD<20030905 OR PD<20030905)

=> d ibib abs 17 1-2

L7 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1999:475033 HCAPLUS

DOCUMENT NUMBER: 131:254599

TITLE: BLEEP-**potential** of **mean**
force describing **protein-**

AUTHOR(S): Mitchell, John B. O.; Laskowski, Roman A.; Alex,
Alexander; Thornton, Janet M.

CORPORATE SOURCE: Department of Biochemistry and Molecular Biology,
University College London, London, WC1H 0AJ, UK

SOURCE: Journal of Computational Chemistry (1999),
20(11), 1165-1176

CODEN: JCCHDD; ISSN: 0192-8651

PUBLISHER: John Wiley & Sons, Inc.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have developed BLEEP (biomol. ligand energy evaluation protocol), an
atomic level **potential** of **mean force** (
PMF) describing **protein-ligand** interactions.
The **pair potentials** for BLEEP have been derived from
high-resolution x-ray structures of **protein-ligand**
complexes in the Brookhaven Protein Data Bank (PDB), with a careful
treatment of homol. The use of a broad variety of **protein-**
ligand structures in the derivation phase gives BLEEP more general
applicability than previous potentials, which have been based on limited
classes of complexes, and thus represents a significant step forward. We
calculate the distance distributions in **protein-ligand**
interactions for all 820 possible pairs that can be chosen from our set of
40 different atom types, including polar hydrogen. We then use a reverse
Boltzmann methodol. to convert these into energy-like **pair**
potential functions. Two versions of BLEEP are calculated, one
including and one excluding interactions between protein and water. The
pair potentials are found to have the expected forms;
polar and hydrogen bonding interactions show min. at short range, around
3.0 A, whereas a typical hydrophobic interaction is repulsive at this
distance, with values above 4.0 A being preferred.

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 1999:122707 HCAPLUS

DOCUMENT NUMBER: 130:320363

TITLE: A General and Fast Scoring Function for
Protein-Ligand Interactions: A
Simplified Potential Approach

AUTHOR(S): Muegge, Ingo; Martin, Yvonne C.

CORPORATE SOURCE: Pharmaceutical Products Division, Abbott Laboratories,
Abbott Park, IL, 60064-6100, USA

SOURCE: Journal of Medicinal Chemistry (1999),
42(5), 791-804

CODEN: JMCMAR; ISSN: 0022-2623

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A fast, simplified potential-based approach is presented that ests. the **protein-ligand** binding affinity based on the given 3D structure of a **protein-ligand** complex. This general, knowledge-based approach exploits structural information of known **protein-ligand** complexes extracted from the Brookhaven Protein Data Bank and converts it into distance-dependent Helmholtz free interaction energies of **protein-ligand** atom pairs (potentials of mean force, **PMF**). The definition of an appropriate reference state and the introduction of a correction term accounting for the volume taken by the ligand were found to be crucial for deriving the relevant interaction potentials that treat solvation and entropic contributions implicitly. A significant correlation between exptl. binding affinities and computed score was found for sets of diverse **protein-ligand** complexes and for sets of different ligands bound to the same target. For 77 **protein-ligand** complexes taken from the Brookhaven Protein Data Bank, the calculated score showed a standard deviation from observed

binding affinities of 1.8 log Ki units and an R2 value of 0.61. The best results were obtained for the subset of 16 serine protease complexes with a standard deviation of 1.0 log Ki unit and an R2 value of 0.86. A set of 33 inhibitors modeled into a crystal structure of HIV-1 protease yielded a standard deviation of 0.8 log Ki units from measured inhibition consts. and an R2 value of 0.74. In contrast to empirical scoring functions that show similar or sometimes better correlation with observed binding affinities, our method does not involve deriving specific parameters that fit the observed binding affinities of **protein-ligand** complexes of a given training set. We compared the performance of the **PMF** score, Bohm's score (LUDI), and the SMOG score for eight different test sets of **protein-ligand** complexes. It was found that for the majority of test sets the **PMF** score performs best. The strength of the new approach presented here lies in its generality as no knowledge about measured binding affinities is needed to derive atomic interaction potentials. The use of the new scoring function in docking studies is outlined.

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d que stat 19

L4 1965 SEA FILE=HCAPLUS ABB=ON ?POTENTIAL?(3W)?MEAN?(W)?FORCE? OR
PMF

L5 26 SEA FILE=HCAPLUS ABB=ON L4 AND ?PROTEIN?(W)?LIGAND?

L6 4 SEA FILE=HCAPLUS ABB=ON L5 AND (?REPULS? OR ?PAIR? OR
?INTERATOM?)(W)?POTENT?

L8 3 SEA L6

L9 1 DUP REMOV L8 (2 DUPLICATES REMOVED)

=> d ibib abs 19 1-1

L9 ANSWER 1 OF 1 MEDLINE on STN DUPLICATE 1

ACCESSION NUMBER: 1999173934 MEDLINE

DOCUMENT NUMBER: PubMed ID: 10072678

TITLE: A general and fast scoring function for **protein-ligand** interactions: a simplified potential approach.

AUTHOR: Muegge I; Martin Y C

CORPORATE SOURCE: Pharmaceutical Products Division, Abbott Laboratories,
Abbott Park, Illinois 60064-6100, USA..
ingo.muegge.b@bayer.comSOURCE: Journal of medicinal chemistry, (1999 Mar 11) 42 (5)
791-804.

Journal code: 9716531. ISSN: 0022-2623.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals; AIDS

ENTRY MONTH: 199904

ENTRY DATE: Entered STN: 19990426

Last Updated on STN: 19990426

Entered Medline: 19990413

AB A fast, simplified potential-based approach is presented that estimates the **protein-ligand** binding affinity based on the given 3D structure of a **protein-ligand** complex. This general, knowledge-based approach exploits structural information of known **protein-ligand** complexes extracted from the Brookhaven Protein Data Bank and converts it into distance-dependent Helmholtz free interaction energies of **protein-ligand** atom pairs (potentials of mean force, PMF). The definition of an appropriate reference state and the introduction of a correction term accounting for the volume taken by the ligand were found to be crucial for deriving the relevant interaction potentials that treat solvation and entropic contributions implicitly. A significant correlation between experimental binding affinities and computed score was found for sets of diverse **protein-ligand** complexes and for sets of different ligands bound to the same target. For 77 **protein-ligand** complexes taken from the Brookhaven Protein Data Bank, the calculated score showed a standard deviation from observed binding affinities of 1.8 log Ki units and an R2 value of 0.61. The best results were obtained for the subset of 16 serine protease complexes with a standard deviation of 1.0 log Ki unit and an R2 value of 0.86. A set of 33 inhibitors modeled into a crystal structure of HIV-1 protease yielded a standard deviation of 0.8 log Ki units from measured inhibition constants and an R2 value of 0.74. In contrast to empirical scoring functions that show similar or sometimes better correlation with observed binding affinities, our method does not involve deriving specific parameters that fit the observed binding affinities of **protein-ligand** complexes of a given training set. We compared the performance of the PMF score,

Bohm's score (LUDI), and the SMOG score for eight different test sets of **protein-ligand** complexes. It was found that for the majority of test sets the **PMF** score performs best. The strength of the new approach presented here lies in its generality as no knowledge about measured binding affinities is needed to derive atomic interaction potentials. The use of the new scoring function in docking studies is outlined.

=> d que stat 110

L4 1965 SEA FILE=HCAPLUS ABB=ON ?POTENTIAL?(3W)?MEAN?(W)?FORCE? OR
PMF

L5 26 SEA FILE=HCAPLUS ABB=ON L4 AND ?PROTEIN?(W)?LIGAND?

L6 4 SEA FILE=HCAPLUS ABB=ON L5 AND (?REPULS? OR ?PAIR? OR
?INTERATOM?)(W)?POTENT?

L10 3 SEA FILE=USPATFULL ABB=ON L6 AND (PRD<20030905 OR PD<20030905)

=> d ibib abs 110 1-3

L10 ANSWER 1 OF 3 USPATFULL on STN

ACCESSION NUMBER: 2003:189033 USPATFULL

TITLE: Protein design automation for protein libraries

INVENTOR(S): Bentzien, Joerg, White Plains, NY, UNITED STATES

Dahiyat, Bassil I., Altadena, CA, UNITED STATES

Desjarlais, John R., Pasadena, CA, UNITED STATES

Hayes, Robert J., Pasadena, CA, UNITED STATES

Vielmetter, Jost, Altadena, CA, UNITED STATES

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003130827	A1	20030710	<--
APPLICATION INFO.:	US 2002-218102	A1	20020812 (10)	
RELATED APPLN. INFO.:	Continuation of Ser. No. US 2001-927790, filed on 10 Aug 2001, PENDING			

	NUMBER	DATE	
PRIORITY INFORMATION:	US 2001-311545P	20010810 (60)	<--
	US 2001-324899P	20010925 (60)	<--
	US 2002-351937P	20020125 (60)	<--
	US 2002-352103P	20020125 (60)	<--
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	ROBIN M. SILVA, DORSEY & WHITNEY LLP, SUITE 3400, FOUR EMBARCADERO CENTER, SAN FRANCISCO, CA, 94111		
NUMBER OF CLAIMS:	116		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	29 Drawing Page(s)		
LINE COUNT:	5782		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to the use of protein design automation (PDA.TM.) to generate computationally prescreened secondary libraries of proteins, and to methods and compositions utilizing the libraries.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L10 ANSWER 2 OF 3 USPATFULL on STN

ACCESSION NUMBER: 2003:189003 USPATFULL

TITLE: Protein modeling tools

INVENTOR(S): Skolnick, Jeffrey, Creve Corner, MD, UNITED STATES

Kolinski, Andrzej, Warsaw, POLAND

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2003130797	A1	20030710	<--
APPLICATION INFO.:	US 2001-982488	A1	20011017 (9)	
RELATED APPLN. INFO.:	Division of Ser. No. US 2000-493022, filed on 27 Jan 2000, PENDING			

	NUMBER	DATE	
	-----	-----	
PRIORITY INFORMATION:	US 1999-117570P	19990127 (60)	<--
	US 1999-118844P	19990205 (60)	<--
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	GREGORY P. EINHORN, Fish & Richardson P.C., Suite 500, 4350 La Jolla Village Drive, San Diego, CA, 92122		
NUMBER OF CLAIMS:	13		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	21 Drawing Page(s)		
LINE COUNT:	4029		
AB	<p>The invention provides a new, efficient method for the assembly of protein tertiary structure from known, loosely encoded secondary structure constraints and sparse information about exact side chain contacts. The method is based on a new method for the reduced modeling of protein structure and dynamics, where the protein is described by representing side chain centers of mass rather than alpha-carbons. The model has implicit, built-in multi-body correlations that simulate short- and long-range packing preferences, hydrogen bonding cooperativity, and a mean force potential describing hydrophobic interactions. Due to the simplicity of the protein representation and definition of the model force field, the Monte Carlo algorithm is at least an order of magnitude faster than previously published Monte Carlo algorithms for three-dimensional structure assembly. In contrast to existing algorithms, the new method requires a smaller number of tertiary constraints for successful fold assembly; on average, one for every seven residues as compared to one for every four residues. The reliability and robustness of the invention make it useful for routine application in model building protocols based on various (and even very sparse) experimentally-derived structural constraints.</p>		

L10 ANSWER 3 OF 3 USPATFULL on STN

ACCESSION NUMBER: 2003:78520 USPATFULL
 TITLE: Novel proteins with integrin-like activity
 INVENTOR(S): Mayo, Stephen, Pasadena, CA, UNITED STATES
 Shifman, Julia, Pasadena, CA, UNITED STATES
 Shimaoka, Motomu, Brookline, MA, UNITED STATES
 Springer, Timothy, Newton, MA, UNITED STATES

	NUMBER	KIND	DATE	
	-----	-----	-----	
PATENT INFORMATION:	US 2003054440	A1	20030320	<--
	US 6951927	B2	20051004	
APPLICATION INFO.:	US 2001-902481	A1	20010709 (9)	

	NUMBER	DATE	
	-----	-----	
PRIORITY INFORMATION:	US 2000-216600P	20000707 (60)	<--
DOCUMENT TYPE:	Utility		
FILE SEGMENT:	APPLICATION		
LEGAL REPRESENTATIVE:	FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT LLP, Suite 3400, Four Embarcadero Center, San Francisco, CA, 94111		
NUMBER OF CLAIMS:	30		
EXEMPLARY CLAIM:	1		
NUMBER OF DRAWINGS:	12 Drawing Page(s)		
LINE COUNT:	3976		

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB The invention relates to novel proteins with novel integrin and I domain

activity and nucleic acids encoding these proteins. The invention further relates to the use of the novel proteins in the treatment of integrin related disorders.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

Zeman 10/655,870

19/01/2006

=> d ibib abs ind l2 1-1

L2 ANSWER 1 OF 2 HCAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2005:220217 HCAPLUS

DOCUMENT NUMBER: 142:276463

TITLE: Calculating a potential of mean force (PMF) score of a **protein-ligand** complex including a repulsion-term module, and potential drug discovery applications

INVENTOR(S): Purvis, George D.

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 9 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----
US 2005055165	A1	20050310	US 2003-655870	20030905
PRIORITY APPLN. INFO.:			US 2003-655870	20030905
AB	To identify a ligand that may have greater binding affinity to a protein associated with the illness, potential mean force (PMF) scores of multiple protein-ligand complexes that each include the protein and one of multiple ligands may be calculated and compared with each other. A PMF score of a protein-ligand complex may indicate the binding affinity between the protein and ligand. A ligand in a protein-ligand complex that has a lower (more neg.) PMF score may be a better candidate for a drug that may be used to treat the illness than a ligand in a protein-ligand complex that has a higher PMF score. A system for calculating a PMF score of a protein-ligand complex includes a repulsion-term module that accesses parameters usable to calculate a repulsion term usable to calculate a PMF of a protein-ligand atom pair in the protein-ligand complex. The parameters correspond to an atom-pair type of the protein-ligand atom pair. The repulsion-term module uses the accessed parameters to calculate the repulsion term usable to calculate the PMF of the protein-ligand atom pair. The repulsion-term module communicates the calculated repulsion term for calcn. of the PMF score of the protein-ligand complex.			
IC	ICM G01N033-48			
	ICS G01N033-50; G01N031-00			
INCL	702019000			
CC	9-16 (Biochemical Methods)			
	Section cross-reference(s): 1, 6			
ST	protein ligand mean force potential repulsion term drug discovery			
IT	Computer application			
	Computer program			
	Drug discovery			
	Interatomic potential			
	Molecular association			
	Molecular mechanics			
	Molecular modeling			
	Pair potential			
	Potential energy			
	Repulsive potential			

(calculating potential of mean force (PMF) score of **protein-ligand** complex including repulsion-term module, and potential drug discovery applications)

IT Ligands

Proteins

RL: PRP (Properties)

(complexes; calculating potential of mean force (PMF) score of **protein-ligand** complex including repulsion-term module, and potential drug discovery applications)

IT Algorithm

(genetic; calculating potential of mean force (PMF) score of **protein-ligand** complex including repulsion-term module, and potential drug discovery applications)

IT Databases

(protein data bank; calculating potential of mean force (PMF) score of **protein-ligand** complex including repulsion-term module, and potential drug discovery applications)